The NEDD8-Activating Enzyme Inhibitor, MLN4924, Cooperates with TRAIL to Augment Apoptosis through Facilitating c-FLIP Degradation in Head and Neck Cancer Cells

Liqun Zhao, Ping Yue, Sagar Lonial, Fadlo R. Khuri, and Shi-Yong Sun

Abstract

TNF-related apoptosis-inducing ligand (TRAIL) is a tumor-selective cytokine with potential anticancer activity and is currently under clinical testing. Head and neck squamous cell carcinoma (HNSCC), like other cancer types, exhibits varied sensitivity to TRAIL. MLN4924 is a newly developed investigational small molecule inhibitor of NEDD8-activating enzyme with potent anticancer activity. This study reveals a novel function of MLN4924 in synergizing with TRAIL to induce apoptosis in HNSCC cells. MLN4924 alone effectively inhibited the growth of HNSCC cells and induced apoptosis. When combined with TRAIL, synergistic effects on decreasing the survival and inducing apoptosis of HNSCC cells occurred. MLN4924 decreased c-FLIP levels without modulating death receptor 4 and death receptor 5 expression. Enforced expression of c-FLIP substantially attenuated MLN4924/TRAIL–induced apoptosis. Thus c-FLIP reduction plays an important role in mediating MLN4924/TRAIL–induced apoptosis. Moreover, MLN4924 decreased c-FLIP stability, increased c-FLIP ubiquitination, and facilitated c-FLIP degradation, suggesting that MLN4924 decreases c-FLIP levels through promoting its degradation. MLN4924 activated c-jun-NH₂-kinase (JNK) signaling, evidenced by increased levels of phospho-c-Jun in MLN4924-treated cells. Chemical inhibition of JNK activation not only prevented MLN4924-induced c-FLIP reduction, but also inhibited MLN4924/TRAIL–induced apoptosis, suggesting that JNK activation mediates c-FLIP downregulation and subsequent enhancement of TRAIL-induced apoptosis by MLN4924. Because knockdown of NEDD8 failed to activate JNK signaling and downregulate c-FLIP, it is likely that MLN4924 reduces c-FLIP levels and enhances TRAIL–induced apoptosis independent of NEDD8 inhibition.

Introduction

TNF-related apoptosis-inducing ligand (TRAIL; also called APO-2L) is a member of the TNF family and is currently being tested in phase I oncology trials based on its unique ability to trigger apoptosis in various types of cancer cells with limited toxicity toward normal cells. Moreover, it is distinct from the death ligands TNFα and Fas, which, in addition to inducing apoptosis in cancer cells, cause severe inflammatory response and liver damage, respectively, when administered systemically (1, 2). However, cancer cells exhibit varied sensitivity to TRAIL, with some possessing intrinsic resistance to TRAIL.

Induction of apoptosis by TRAIL involves its initial binding to death receptor 4 (DR4) or 5 (DR5), oligomerization of the death receptors, and formation of the death-inducing signaling complex (DISC), involving recruitment of the adaptor molecule FADD and subsequent activation of the effector caspases (e.g., caspase-3) that eventually drive apoptotic death (3). Cellular FLICE-inhibitory protein (c-FLIP) is a truncated form of caspase-8 that lacks enzymatic activity. In addition to functioning as a decoy receptor, c-FLIP also has the ability to inhibit the activation of effector caspases, and it has been shown that elevated c-FLIP expression is associated with resistance to TRAIL-induced apoptosis, whereas downregulation of c-FLIP by pharmacological or RNAi approaches sensitize cells to death receptor-mediated apoptosis (4, 5). Therefore, c-FLIP acts as a key inhibitor of TRAIL/death receptor-mediated apoptosis.
receptor–induced apoptosis. c-FLIP has multiple isoforms; however, only 2 forms have been well characterized at the protein level: short form (c-FLIP_S) and long form (c-FLIP_L; ref. 4).

Ubiquitination is a well-known posttranslational protein modification process that mediates proteasome-dependent degradation of many intracellular proteins. c-FLIP is known to be regulated by such a process and thus is a rapidly turned over protein (6, 7). Certain cancer therapeutic agents stimulate downregulation of c-FLIP expression through this mechanism (6, 8–10). However, the mechanism underlying drug-induced c-FLIP degradation is unclear. A recent study has shown that c-Jun-NH2-kinase (JNK)-mediated activation of the E3 ubiquitin ligase Itch specifically ubiquitinates c-FLIP_L and induces its proteasomal degradation (11).

Neddylation is a homologous pathway to ubiquitination. The NEDD8 protein is the closest to ubiquitin and can also be conjugated to target proteins (12). To date, a number of targets have been identified and most belong to cullin family. Cullin proteins have been reported to act as core scaffolds for the assembly of cullin-RING E3 ligases (CRL), which is the largest family of ubiquitin E3 ligases comprising several hundred members (13). The neddylation of cullins by NEDD8 results in activation of CRLs by facilitating the recruitment and positioning of ubiquitin E2 enzyme (14, 15). Therefore, the neddylation process is involved in the function of a variety of molecules by regulating their degradation through ubiquitination modification (15). Neddylation has been shown to play an essential role in cellular survival and thus is involved in diseases such as cancer (15, 16). Consequently, efforts have been made to target protein neddylation for cancer therapy. MLN4924 is a recently identified small molecule that inhibits NEDD8-activating enzyme (17, 18). Preclinical studies have shown that MLN4924 has anticancer activities against a wide range of tumors. It has recently been shown that highly proliferative head and neck squamous cell carcinoma (HNSCC) cells possess upregulated NEDD8 conjugation (19). However, the activity of MLN4924 against HNSCC cells has not been reported. In this report, we studied the single agent activity of MLN4924 against HNSCC cells has not been reported. By analyzing short-tandem repeat DNA profile. The other cell lines have not been authenticated.

Establishment of stable HNSCC lines expressing ectopic LacZ, FLIPL, and FLIPS

22A and Tr146 cells were infected with lentiviruses carrying LacZ, FLIPL, and FLIPS as described previously (8). The blasticidin screening concentrations were 6.25 μg/mL and 10 μg/mL for 22A and Tr146, respectively.

Cell survival and apoptosis assays

Cells were seeded in 96-well cell culture plates and were treated the next day with the given agents. The viable cell number was determined using sulforhodamine B (SRB) assay as described previously (22). Combination index (CI) for drug interaction (e.g., synergy) was calculated using the CompuSyn Software (ComboSyn, Inc.). Apoptosis was evaluated with the Annexin V-PE Apoptosis Detection Kit purchased from BD Biosciences. We also detected caspase and PARP cleavage by Western blot analysis as described below, as additional indicators of apoptosis.

Western blot analysis

Whole-cell protein lysates were prepared as described before (23, 24). Protein concentration was determined with the Bio-Rad Protein Assay Kit. Protein was electrophoresed through polyacrylamide gels and transferred to PVDF membranes (Bio-Rad). Blots were probed with primary antibodies followed by secondary antibodies. Eventually, antibody signal was detected using the enhanced chemiluminescence system (Thermo Scientific) according to the manufacturer’s directions.
Immunoprecipitation for detection of ubiquitinated c-FLIP
Tr146–FLIPL cells were transfected with hemagglutinin (HA)-ubiquitin plasmid using the Lipofectamine 2000 Transfection Reagent (Invitrogen) based on the manufacturer’s instructions. After 24 hours, the cells were subjected to estimation of cell number using the SRB assay. Points, means of 4 replicate determinations; bars, ±SD. B and C, the given cell lines were treated with the indicated concentrations of MLN4924 for 48 hours and then harvested for detection of caspase-3 and PARP cleavage (B) and apoptosis (C) with Western blot analysis and Annexin V staining, respectively. Columns, means of duplicate determinations; bars, ±SD.

siRNA-mediated gene knockdown
Itch siRNA (5'-AAGTGCTTCTCAGAATGATGA-3') was synthesized by Qiagen. NEDD8 siRNA, which is a pool of 3 target-specific siRNAs (sc-36026), was purchased from Santa Cruz Biotechnology, Inc. Transfection of these siRNA duplexes was conducted in 6-well plates using the HiPerFect Transfection Reagent (Qiagen) following the manufacturer’s manual. Gene-silencing effects were evaluated by Western blot analysis.

Results
MLN4924 effectively induces apoptosis of human HNSCC cells
The single agent activity of MLN4924 on the growth of HNSCC was evaluated. A 48-hour treatment with MLN4924 effectively inhibited the growth of a panel of HNSCC cell lines including 22B, Tr146, 22A, 1483, SqCC/Y1, 686Ln, and 17B (Fig. 1A). The inhibitory concentrations that decreased cell numbers by 50% (IC50s) ranged between 50 and 600 µmol/L (Fig. 1A). Thus, MLN4924 effectively inhibits the growth of HNSCC cells, albeit to various degrees.

To determine whether the reduced cell number was caused by apoptosis, we treated 2 HNSCC cell lines, Tr146 and SqCC/Y1, with different concentrations of MLN4924 for 48 hours and then detected apoptosis with both Western blot analysis and Annexin V staining in these cells. Two apoptotic markers, cleaved PARP and caspase-3, were concomitantly increased (Fig. 1B). Moreover, increased Annexin V–positive cell populations (10%–60%) were detected in a dose-dependent manner in both cell lines in comparison with untreated control cells (Fig. 1C). These results collectively indicate that MLN4924 potently induces apoptosis. Thus we conclude that MLN4924 decreases the numbers of HNSCC cells through induction of apoptosis.

MLN4924 cooperates with TRAIL to enhance apoptosis
Similar to other types of cancer, some HNSCC cell lines (e.g., 22A, Tr146, SqCC/Y1, and 686Ln) were intrinsically insensitive to TRAIL (Supplementary Fig. S2). We were interested in enhancing TRAIL-induced apoptosis and thus we determined whether MLN4924 has the ability to enhance TRAIL-induced apoptosis in these insensitive HNSCC cell lines. As
The combination of MLN4924 and TRAIL synergistically decreased cell survival (A), enhances cleavage of caspases (B), and induces apoptosis (C). A, the given cell lines were plated on 96-well plates and treated the next day with the given doses of TRAIL alone, MLN4924 (MLN) alone, or their combinations. After 24 hours, cell numbers were estimated using the SRB assay. Columns, means of 4 replicated determinations; bars, ±SD. The numbers labeling the lines in the graphs are CIs. B and C, the given cell lines were treated with 40 ng/mL TRAIL alone, 1 µmol/L MLN4924 alone, and their combination. After 24 hours, the cells were harvested for preparation of whole-cell protein lysates and subsequent Western blot analysis (B) and for Annexin V staining of apoptosis (C). Columns, means of duplicate determinations; bars, ±SD. CF, cleaved form.

**MLN4924 reduces c-FLIP levels in HNSCC cells**

To reveal the mechanism by which MLN4924 enhances TRAIL-initiated apoptosis, we analyzed alterations of several key proteins including c-FLIP, DR4, DR5, DcR1, and DcR2 in the TRAIL/death receptor–mediated apoptotic pathway in cells exposed to MLN4924. We also detected the expression of p27, an essential cell-cycle inhibitor, that is known to be a CRL substrate and is used as a marker to show the effectiveness of MLN4924 in inhibiting protein neddylation as previously reported (16, 17). As expected, MLN4924 treatment resulted in substantial accumulation of p27 in all 3 HNSCC cell lines (SqCC/Y1, Tr146, and 22A) tested, suggesting that MLN4924 at the tested concentration range (0.25–2 µmol/L) indeed inhibits protein neddylation. With the same concentration range, MLN4924 exerted dose-dependent effects on reducing c-FLIP levels, but had minimal effects on increasing the levels of DR4 and DR5 (Fig. 3A). MLN4924 even at 0.25 µmol/L effectively reduced the levels of c-FLIP (both FLIP L and FLIPS) in some cell lines (e.g., SqCC/Y1). Time course analysis showed that c-FLIP (both FLIP L and FLIPS) reduction occurred after 6-hour treatment with MLN4924; this reduction was sustained up to 15 hours in both SqCC/Y1 and Tr146 cells. Within the tested period, MLN4924 did not alter the levels of...
either DR4 or DR5 (Fig. 3B). In both SqCC/Y1 and 22A cell lines, we failed to detect the expression of DcR1 and DcR2 even in the presence of MLN4924 (Supplementary Fig. S3). Thus, it is clear that MLN4924 reduces c-FLIP levels without altering the expression of DR4, DR5, DcR1, and DcR2.

Moreover, we analyzed the effects of MLN4924 on the expression of several other proteins (e.g., Bcl-2 family proteins and inhibitors of apoptosis) associated with regulation of TRAIL-induced apoptosis. As shown in Supplementary Fig. S4, MLN4924 reduced the levels of survivin, but did not alter the expression of Bax, Bcl-XL, Mcl-1, and XIAP in both SqCC/Y1 and 22A cell lines. Interestingly, MLN4924 did not affect Bcl-2 expression in 22A cells, but increased its expression in SqCC/Y1 cells, although we did not know the biological significance of bcl-2 upregulation in this cell line.

**Enforced expression of ectopic c-FLIP protects HNSCC cells from induction of apoptosis by the MLN4924 and TRAIL combination**

To explore the role of c-FLIP downregulation in apoptosis induction by MLN4924 plus TRAIL, we established stable 22A and Tr146 cell lines that expressed ectopic FLIP L and FLIP S. These cell lines were characterized by Western blot analysis to ensure successful expression of the given forms of c-FLIP (Fig 4A). Upon establishment of these cell lines, we compared their responses with the combination of MLN4924 and TRAIL. The combination of MLN4924 and TRAIL was more effective than either agent alone in decreasing the survival of 22A–LacZ cells, but not of 22A–FLIP L or 22A–FLIP S cells. Similarly, the combination of MLN4924 and TRAIL effectively decreased the survival of Tr146–Lac Z cells; but this effect was attenuated in Tr146–FLIP L and Tr146–FLIP S cells (Fig. 4B). The combination of MLN4924 and TRAIL was much more effective in inducing the cleavage of caspase-8, caspase-9, caspase-3, and PARP in 22A–LacZ cells than in 22A–FLIP S and 22A–FLIP L cells (Fig. 4C). In agreement, the MLN4924 and TRAIL combination caused 32% apoptosis in 22A–LacZ cells, but only 16% and 19% apoptotic cells, respectively, in 22A–FLIP S and 22A–FLIP L cells (Fig. 4D). These data taken together indicate that overexpression of c-FLIP protects cells from apoptosis induced by the MLN4924 and TRAIL combination.
combination, implying that c-FLIP downregulation contributes to the enhancement of TRAIL-induced apoptosis by MLN4924.

**MLN4924 downregulates c-FLIP through facilitating ubiquitin/proteasome–mediated degradation**

To reveal the mechanism by which MLN4924 reduces c-FLIP levels, we first tested whether proteasomal degradation is involved in this process, as c-FLIP is known to be regulated by a ubiquitin/proteasome–dependent mechanism. Thus, we treated SqCC/Y1 cells with MLN4924 in the absence and presence of the proteasome inhibitor MG132 and then detected c-FLIP with Western blot analysis. In the absence of MG132, MLN4924 decreased c-FLIP levels as we showed before. However, the presence of MG132 increased basal levels of c-FLIP, particularly FLIPS and prevented c-FLIP from reduction by MLN4924 (Fig. 5A). These data suggest that MLN4924 induces c-FLIP reduction through a proteasome-dependent mechanism. We next determined whether MLN4924 increases c-FLIP ubiquitination. As presented in Fig. 5C, the highest level of ubiquitinated FLIPS was detected in cells treated with MLN4924 plus MG132 compared with MLN4924 alone or MG132 alone, indicating that MLN4924 increases c-FLIP ubiquitination. Collectively, we conclude that MLN4924 facilitates ubiquitin/proteasome–mediated c-FLIP degradation, leading to the downregulation of c-FLIP protein level.

**MLN4924-induced JNK activation mediates c-FLIP downregulation independent of Itch**

It was reported that JNK activation can lead to FLIPS degradation involving the E3 ligase Itch (11). Thus we asked whether JNK and Itch are involved in mediating MLN4924-induced c-FLIP degradation. To this end, we first determined whether MLN4924
activates JNK signaling. MLN4924 at the tested concentrations ranging from 0.25 to 2 μmol/L substantially increased phosphorylation of c-Jun, a well-known substrate of JNK, in a dose-dependent manner in both Tr146 and SqCC/Y1 cells (Fig. 6A). The increase in p-c-Jun occurred at 3 hours (Tr146) or at 6 hours (SqCC/Y1) and was sustained for up to 15 hours (Fig. 6B). Moreover, we noted that the total levels of c-Jun were apparently increased in SqCC/Y1 cells. Thus, these data clearly indicate that MLN4924 rapidly and potently activates JNK signaling. To explore the relationship between JNK activation and c-FLIP downregulation, we treated SqCC/Y1 cells with MLN4924 in the absence and presence of the JNK-specific inhibitor, SP600125, and then compared c-FLIP expression under these conditions. As shown in Fig. 6C, MLN4924 could increase the levels of p-c-Jun and c-Jun and reduce the levels of c-FLIP in the absence of SP600125, but failed to do so in the presence of SP600125. Thus SP600125 abolishes MLN4924’s ability to reduce c-FLIP levels, suggesting that JNK activation mediates c-FLIP downregulation induced by MLN4924. Furthermore, we inhibited Itch by knocking down its expression and then examined its impact on MLN4924-induced c-FLIP downregulation. As shown in Fig. 6D, transfection of Itch siRNA substantially reduced the levels of Itch, indicating the successful knockdown of Itch expression. However, MLN4924 still decreased the levels of FLIP_L and FLIP_S in Itch siRNA–transfected cells to the same degree as in control siRNA–transfected cells, indicating that Itch inhibition failed to affect the ability of MLN4924 to downregulate c-FLIP. Thus, it appears that MLN4924 downregulates c-FLIP independent of Itch.

JNK inhibition protects HNSCC cells from MLN4924/TRAIL–induced apoptosis

To further unravel the role of JNK in MLN4924/TRAIL–induced apoptosis, we also tested the impact of JNK inhibition on cooperative induction of apoptosis by the MLN4924 and TRAIL combination. The MLN4924 and TRAIL combination apparently induced cleavage of caspase-8, caspase-9, caspase-3, and PARP in the absence of SP600125, but only minimally in the presence of SP600125 (Fig. 6E). In agreement, the combination of MLN4924 and TRAIL was much more potent than either agent alone in induction of apoptosis (up to 45%) in the absence of SP600125. However, the combination induced only approximately 15% apoptosis in the presence of SP600125 (Fig. 6F). Collectively, these data indicate that inhibition of JNK substantially attenuates MLN4924’s ability to enhance TRAIL-induced apoptosis.
Knockdown-mediated inhibition of NEDD8 does not downregulate c-FLIP and activate JNK

To know whether MLN4924-induced c-FLIP downregulation is a consequence of protein neddylation inhibition, we asked whether we can generate a similar reduction in c-FLIP levels by directly inhibiting NEDD8 through gene silencing. The data shown in Supplementary Fig. S5A show that transfection of NEDD8 siRNA into 2 HNSCC cell lines (SqCC/Y1 and Tr146) and 2 lung cancer cell lines that express high levels of c-FLIP (A549 and H157) substantially reduced the levels of NEDD8, but did not decrease c-FLIP levels in any of the cell lines. Thus, inhibition of NEDD8 with siRNA does not mimic MLN4924 in downregulating c-FLIP expression. Moreover, we failed to detect increased levels of p-c-Jun and c-Jun in NEDD8 siRNA–transfected cells (Supplementary Fig. S5B), indicating that NEDD8 inhibition does not mimic MLN4924 in activating JNK signaling either.

Discussion

In this study, we have shown that MLN4924 effectively inhibits the growth of a panel of HNSCC cell lines with IC50s ranging from 50 nmol/L to 600 nmol/L. Moreover, MLN4924 potently induces apoptosis of HNSCC cells (Fig. 1). Thus our findings warrant further
and enhancement of TRAIL-induced apoptosis in HNSCC. Moreover, we have shown that MLN4924, when combined with TRAIL, synergistically decreased the survival and induced apoptosis of HNSCC cells (Fig. 2). To the best of knowledge, this is the first report of the cooperative induction of apoptosis between MLN4924 and TRAIL. Given that TRAIL is being tested as a cancer therapeutic agent in clinical trials (3, 26), the further study of the potential application of MLN4924 and TRAIL combination in cancer therapy (e.g., HNSCC) is also warranted.

DR4, DR5, DcR1, DcR2, and c-FLIP are key components in the regulation of TRAIL-induced apoptosis: DR4, DR5, DcR1, and DcR2 are receptors for TRAIL that initiate (i.e., DR4 and DR5) or inhibit (i.e., DcR1 and DcR2) apoptosis upon binding with TRAIL and c-FLIP is the major inhibitor that suppresses TRAIL/death receptor–induced apoptosis (3, 27). Modulation of the levels of these proteins in general results in sensitization of cancer cells to TRAIL-induced apoptosis (28, 29). In this study, MLN4924 reduced the levels of c-FLIP without increasing DR4 or DR5 expression (Fig. 2). Moreover, we did not detect the expression of DcR1 and DcR2 in the absence and presence of MLN4924 in the tested HNSCC cell lines (Supplementary Fig. S3). These results indicate that MLN4924 primarily reduces c-FLIP levels in HNSCC cells. Enforced expression of ectopic FLIP\textsubscript{L} or FLIP\textsubscript{S} conferred resistance of HNSCC cells to the combination of MLN4924 and TRAIL, as evaluated by cell survival and apoptosis assays (Fig. 4). Therefore, c-FLIP downregulation apparently plays a critical role in mediating synergistic induction of apoptosis by MLN4924 and TRAIL. We noted that enforced expression of ectopic c-FLIP failed to provide a completely protective effect against cell killing by the MLN4924 and TRAIL combination (e.g., Tr146 in Fig. 4). Thus we suggest that other mechanisms in addition to c-FLIP downregulation may also contribute to MLN4924-mediated enhancement of TRAIL-induced apoptosis in some cell lines.

In addition to TRAIL receptors and c-FLIP, other proteins such as Bcl-2 family proteins and inhibitors of apoptosis (e.g., XIAP and survivin) are also involved in regulation of TRAIL-induced apoptosis (30). In this study, we have not fully addressed how c-FLIP is degraded by MLN4924; this should be further investigated. The stability of c-FLIP protein (Fig. 5). Thus, it is clear that MLN4924 reduces c-FLIP levels by facilitating its degradation through the ubiquitin/proteasome–dependent pathway. JNK was reported to mediate FLIP\textsubscript{L} degradation through an Itch-dependent mechanism (11). In our study, MLN4924 rapidly and potently activates JNK, as evidenced by increased levels of p-c-Jun in cells exposed to MLN4924 (Fig. 6). We noted that JNK activation occurred at 6 hours post-MLN4924 treatment (Fig. 6), whereas c-FLIP reduction was detected beyond 6 hours (e.g., at 9 hours) post-MLN4924 treatment (Fig. 2). Thus, MLN4924-induced JNK activation occurs ahead of c-FLIP downregulation. Moreover, JNK inhibition with SP600125 abrogated the ability of MLN4924 to decrease c-FLIP levels and to enhance TRAIL-induced apoptosis (Fig. 6). Collectively, we conclude that MLN4924 activates JNK signaling, leading to downregulation of c-FLIP and subsequent enhancement of TRAIL-induced apoptosis. However, we failed to show an involvement of Itch in this event because knockdown of Itch did not prevent MLN4924 from decreasing c-FLIP levels (Fig. 6). This finding may be logical because Itch was suggested to be involved in FLIP\textsubscript{L} degradation (11), whereas MLN4924 downregulates the levels of both FLIP\textsubscript{L} and FLIP\textsubscript{S}.

Because MLN4924 is a NEDD8-activating enzyme inhibitor, we were interested in knowing whether c-FLIP downregulation by MLN4924 is a consequence of specific inhibition of protein neddylation. If so, we would expect that inhibition of NEDD8 with siRNA should generate a similar effect as MLN4924 on c-FLIP and JNK activation. In our study, transfection of NEDD8 siRNA substantially reduced NEDD8 expression, but did not reduce c-FLIP levels in any cell lines tested (Supplementary Fig. S5) or sensitize HNSCC cells to TRAIL-induced apoptosis (data not shown). Moreover, NEDD8 knockdown failed to activate JNK signaling as it did not increase the levels of p-c-Jun (Supplementary Fig. S5). MLN4924 at the tested concentration range (0.25–2 \textmu mol/L) substantially increased the levels of p27 (Fig. 2), a CRL substrate known to be regulated by MLN4924 (17), indicating that MLN4924 sufficiently inhibits protein neddylation at the concentration range tested for downregulation of c-FLIP and enhancement of TRAIL-induced apoptosis. Thus we suggest that either inhibition of NEDD8 or protein neddylation alone is not sufficient to downregulate c-FLIP, or that MLN4924 reduces c-FLIP levels and enhances TRAIL-induced apoptosis independent of NEDD8 inhibition.

In this study, we have not fully addressed how c-FLIP is degraded by MLN4924; this should be further investigated. The stability of c-FLIP has been suggested to be regulated by PKC or Akt through phosphorylation of c-FLIP (32, 33). Whether MLN4924 induces c-FLIP degradation through an off-target mechanism (e.g., by inhibiting these kinases) also needs further investigation.
In addition, c-FLIP expression is known to be positively regulated by NF-κB (34). MLN4924 has been shown to inhibit NF-κB activation in lymphoma and leukemia cells (35, 36). Bcl-2, Bcl-xl, and XIAP, and survival are also NF-κB-regulated genes (37). In this study, MLN4924 did not inhibit the expression of Bcl-2, Bcl-xl, and XIAP, although it reduced the levels of survivin (Supplementary Fig. S4). Nonetheless, it will be interesting to further determine whether inhibition of NF-κB is involved in downregulation of c-FLIP by MLN4924.

In summary, the current work has shown the single-agent activity of MLN4924 against the growth of HNSCC cells including induction of apoptosis. Moreover, MLN4924 sensitizes HNSCC cells to TRAIL-induced apoptosis by enhancing JNK-dependent and ubiquitin/proteasome-mediated c-FLIP degradation. This effect is likely independent of IκB and NEDD8 inhibition. Thus, our findings highlight a novel mechanism by which MLN4924 modulates apoptosis and exerts its anticancer activity and also warrant further study to explore the combination of MLN4924 and TRAIL for potential cancer therapy in the clinic.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Acknowledgments

The authors thank Dr. A. Hammond for editing the manuscript.

Grant Support

The study was supported by Georgia Cancer Coalition Distinguished Cancer Scholar award (S.-Y. Sun) and National Cancer Institute NIH SPORE P50 grant CA128613 (project 2, S.-Y. Sun and F.R. Khuri). The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked advertisement in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

Received June 3, 2011; revised August 29, 2011; accepted September 7, 2011; published OnlineFirst September 12, 2011.

References


The NEDD8-Activating Enzyme Inhibitor, MLN4924, Cooperates with TRAIL to Augment Apoptosis through Facilitating c-FLIP Degradation in Head and Neck Cancer Cells

Liqun Zhao, Ping Yue, Sagar Lonial, et al.

Mol Cancer Ther Published OnlineFirst September 13, 2011.

Updated version
Access the most recent version of this article at:
doi:10.1158/1535-7163.MCT-11-0401

Supplementary Material
Access the most recent supplemental material at:
http://mct.aacrjournals.org/content/suppl/2011/09/22/1535-7163.MCT-11-0401.DC1

E-mail alerts
Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions
To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions
To request permission to re-use all or part of this article, contact the AACR Publications Department at permissions@aacr.org.